

Claims

1. Method for increasing the production of cysteine, glutathione and methionine, and of sulphur derivatives thereof, by plant cells and plants, the
 5 said method consisting in overexpressing an SAT in plant cells and plants containing the said plant cells.

2. Method according to claim 1, characterized in that the SAT which is overexpressed in plant cells is a cysteine-sensitive SAT.

10 3. Method according to claim 2, characterized in that the SAT is a plant SAT or a native SAT of bacterial origin.

15 4. Method according to claim 1, characterized in that the SAT which is overexpressed in plant cells is a cysteine-insensitive SAT.

5. Method according to claim 4, characterized in that the SAT is a plant SAT or an SAT of bacterial origin, or a mutated plant SAT, rendered cysteine-insensitive by mutagenesis.

20 6. Method according to ^{claim 1} ~~one of claims 1 to~~ 5, characterized in that the SAT is overexpressed in the cytoplasm of plant cells.

25 7. Method according to claim 6, characterized in that the SAT is an SAT of bacterial origin.

8. Method according to claim 6, characterized in that the SAT is a plant cytoplasmic SAT, in particular from *Arabidopsis thaliana*.

10. Method according to claim 6,

5 characterized in that the SAT is a non-cytoplasmic
plant SAT from which has been removed its signal(s) for
addressing to cellular compartments other than the
cytoplasm.

11. Method according to claim 10,

10 characterized in that the SAT is SAT1' which is
represented by SEQ ID NO 2.

12. Method according to ~~one of claims 1 to~~ ^{claim 1}

~~-5, characterized in that the SAT is overexpressed in mitochondria.~~

15 13. Method according to claim 12,
22 characterized in that the SAT is overexpressed in the
cytoplasm in the form of a signal peptide/SAT fusion
protein, the mature functional SAT being released
inside mitochondria.

20 14. Method according to claim 13,
characterized in that the mitochondrial addressing
signal peptide consists of at least one signal peptide
from a natural plant protein which is located in
mitochondria, such as for example, the SAT1 signal
25 peptide which is represented by amino acids 1 to 63 in
SEQ ID NO 3.

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20. Method according to claim 19,
characterized in that the SAT is homologous with the
transit peptide.

21. Method according to claim 20,
characterized in that the SAT is a chloroplast SAT of
plant origin, in particular from *Arabidopsis thaliana*.

Sub A1
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claim 23

15 26. Method according to claim 25,
characterized in that the transit peptide consists of a
plant EPSPS transit peptide or a plant RuBisCO ssu
transit peptide.

Claim 25

28. Method according to claim 27,
characterized in that the portion of sequence comprises

~~Claim 27~~

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Sub A 2²⁰

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comprises at least one nucleic acid sequence which encodes an SAT.

35. Chimeric gene according to claim 34,
characterized in that the host organism is chosen from
5 bacteria, for example *E. coli*, yeasts, in particular of
the genera *Saccharomyces*, *Kluyveromyces* or *Pichia*,
fungi, in particular *Aspergillus*, baculoviruses, or
plant cells and plants.

36. Chimeric gene according to claim 35,
10 characterized in that the host organism is a plant cell
or a plant which contains it .

37. Chimeric gene according to claim 36,
characterized in that the 5' regulatory element
comprises regulatory sequences which are promoters in
15 plant cells and plants, and are chosen from promoters
which are expressed in plant leaves, constitutive
promoters, or light-dependent promoters of bacterial,
viral or plant origin.

38. Chimeric gene according to claim 36,
20 characterized in that the 5' regulatory element
comprises regulatory sequences which are promoters in
plant cells and plants, and are chosen from seed-
specific promoters.

39. Chimeric gene according to claim 38,
25 characterized in that the promoter is chosen from the
promoters for napin, phaseolin, glutenin, zein,
helianthinin, albumin and oleosin.

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claim 43

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46. Method according to claim 45,

48. Method according to claim 47,
5 characterized in that the host organism is a
monocotyledonous plant, in particular chosen from
cereals, sugar cane, rice and maize, or a
dicotyledonous plant, in particular chosen from
tobacco, soybean, rape, cotton, beet and clover.

sub A7

Sub A8

Sub A9

Sub A10

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and/or crossing of regenerated plants, according to claim 53.

a 55. Genetically modified plant according to Claim 52
~~one of claims 52 to 54~~, characterized in that it is a
 5 monocotyledonous plant, in particular chosen from
 cereals, sugar cane, rice and maize, or a
 dicotyledonous plant, in particular chosen from
 tobacco, soybean, rape, cotton, beet and clover.

10 56. Genetically modified plant according to Claim 52
~~one of claims 52 to 55~~, characterized in that it
 comprises other genes of interest.

57. Genetically modified plant according to
 claim 56, characterized in that it comprises at least
 one other gene which modifies the content and quality
 15 of the proteins of the said plant, in particular in the
 leaves and/or seeds.

58. Genetically modified plant according to
 either of claims 56 and 57, characterized in that the
 gene encodes a protein enriched in sulphur-containing
 20 amino acids.

a 59. Seeds of genetically modified plants
 according to Claim 52
~~one of claims 52 to 58~~.

add C 25
 add 54